

OF BEING AN EMAIL TO RECEIVEDS.D.C.:



SO	SEQUENCE	666 AA;	7423 MW;	AD3AE56B5EEB194 CRC64;
FT	CARBOHYD	105	105	N-LINKED (GLCNAC. . .) (PROBABLE)
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (PROBABLE)
FT	CARBOHYD	258	258	N-LINKED (GLCNAC. . .) (PROBABLE)
FT	CARBOHYD	330	330	N-LINKED (GLCNAC. . .) (PROBABLE)
FT	CARBOHYD	602	602	N-LINKED (GLCNAC. . .) (PROBABLE)
SO	SEQUENCE	666 AA;	7423 MW;	AD3AE56B5EEB194 CRC64;

Query Match	89.5%;	Score 1897;	DB 1;	Length 666;
Best Local Similarity	90.2%;	Pred. NO. 6.9e-154;		
Matches 358; Conservative	8;	Mismatches 27;	Indels 4;	Gaps 2

QY	1	MTPEPPGSAASAPRARVLSLPAEFGGLPRLRLLLFVVAASAOQSRSRGPRLSAWK -	59
Db	1	MTPEPPGSAASAPRARVPCGPAPRLCLPRLRLLLLMAAASOGHRRSGPRLFAAWK	60
QY	60	--GODHVFQSPPEHTVLFHEPGSFSSVWVGGRGVYHNEPPEGNASRYVNIIGSTKGSC	114
Db	61	HVGQDRVDFQGTTEHTVLFHEPGSSSVWVGGRGVYLFDFPEGKNASRYVNIIGSTKGSC	120
QY	118	ODKODCGNYITLLEBRGNGLLVCGTNAKPSCMNLVNDSSVMSLGEKGYAPESPDENSL	177
Db	121	LDKRDCENYIILLERRSEGLLACCTNARHPSCMNLVNGTV - PLGEMGRYAPFESDENSL	179
QY	178	VLFESGDEVYSTIRKQVNGKIPRRRRIRGSESLTSPDTVMNPOFIATYIHQOAYDDK	233
Db	180	VLFESGDEVYSTIRKQVNGKIPRRRRIRGSESLTSPDTVMNPOFIATYIHQOAYDDK	233
QY	238	IYFFREDNPKNPEAPLNTSVRVVOLCGDQGGESSLSVSKWNFTLKMELCSPDAATNRN	297
Db	240	IYFFREDNPKNPEAPLNTSVRVVOLCGDQGGESSLSVSKWNFTLKMELCSPDAATIKN	299
QY	298	FNRLQDVFLLDPGSGQWEDTRVYGVFSNPWVYSAVCYSLGDDIDRVFTSSLKGYHMLGS	357
Db	300	FNRLQDVFLLDPGSGQWEDTRVYGVFSNPWVYSAVCYSLGDDIDRVFTSSLKGYHSLP	358
QY	358	NPREGKCLPKQKPPIPTETFOYADSHPEYAKQVPEMPG	394
Db	360	NPREGKCLPKQKPPIPTETFOYADSHPEYAKQVPEMPG	396

RESULT 3			
SMAD_MOUSE			
ID	SMAD_MOUSE	STANDARD:	PRT: 861 AA.
AC	009126;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Semaphorin 4D precursor (Semaphorin J) (Sema J) (Semaphorin C-like 2) (M-Sema G).		
DE	SEMA4D OR SEMAJ OR SEMACL2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6; TISSUE=Brain;		
RX	MEDLINE=91125976; PubMed=8969198;		
RA	Fuuyama T., Inagaki S., Kosugi A., Noda S., Saitoh S.-I., Ogata M.,		
RA	Iwahasbi Y., Miyazaki N., Hamoka T., Toiyama M.;		
RT	"identification of a novel transmembrane semaphorin expressed on lymphocytes.";		
RL	J. Biol. Chem. 271:33376-33381(1996).		
CC	-1- FUNCTION: MAY PLAY A FUNCTIONAL ROLE IN THE IMMUNE SYSTEM, AS WELL AS IN THE NERVOUS SYSTEM.		
CC	-1- SUBCELLULAR LOCATION: type I membrane protein.		
CC	-1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN LYMPHOID TISSUES, ESPECIALLY IN THE THYMUS, AS WELL AS IN THE NERVOUS TISSUES.		
CC	-1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.		
CC	-1- SIMILARITY: CONTAINS 1 SEMA DOMAIN.		
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.		
CC	-----		
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DR EMBL;169535: AAC52964.1; -.  
DR MGP; MGI:109244; Sema4d.  
DR InterPro; IPR003306; 1g\_MHC.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR003659; Plexin-1Lke.  
DR InterPro; IPR002165; Plexin\_repeat.  
DR InterPro; IPR001627; Sema.  
DR Pfam; PF00047; Ig; 1.  
DR Pfam; PF01403; Sema; 1.  
DR Pfam; PF01437; PSI; 1.  
DR SMART; SM00408; IGC2; 1.  
DR SMART; SM00423; PSI; 1.  
KW Signal; Transmembrane protein; Multi-pass protein.  
KW Neurogenesis; Developmental protein; Glycoprotein.

FT	SIGNAL	1	23	POTENTIAL.
FT	CHAIN	24	861	SEMAPHORIN 4D.
FT	DOMAIN	24	733	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	734	754	POTENTIAL.
FT	DOMAIN	755	861	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	228	523	SEMA.
FT	DOMAIN	569	630	IG-LIKE C2-TYPE DOMAIN.
FT	DISULFID	576	624	BY SIMILARITY.
FT	CARBOHYD	49	77	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	77	77	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	191	191	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	379	379	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	419	419	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	613	613	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	632	632	N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ	SEQUENCE	861 AA;	9514 MW;	533CD6D271A6D79B CRC64;

Query Match	18.48;	Score 389.5;	DB 1;	Length 861;
Best Local Similarity	29.38;	Pred. NO. 3e-25;		
Matches 128; Conservative	59;	Mismatches 151;	Indels 99;	Gaps 20;

[illegible]

DB	391	1QFVKDHP	LMDDSVTPI	407
RESULT 4				
SM3B_HUMAN		STANDARD:	PRT;	749 AA.
ID	013214	093018;		
AC	30-MAY-2000	(Rel. 39, created)		
DT	30-MAY-2000	(Rel. 39, last sequence update)		
DT	16-OCT-2001	(Rel. 40, last annotation update)		
DE	Semaphorin 3B precursor (Semaphorin V) (Sema V).			
GN	SEMA3B OR SEMA5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEJLNE96210603; PubMed=8633026;			
RA	Sekido Y., Bader S., Latif F., Chen J.-Y., Duh F.-M., Wei M.-H.,			
RA	Albanesi J.P., Lee C.-C., Lerman M.I., Minna J.D.;			
RT	"Human semaphorins A(V) and IV reside in the 3p21.3 small cell lung			
RT	cancer deletion region and demonstrate distinct expression patterns.,"			
RL	Proc. Natl. Acad. Sci. U.S.A. 93:4120-4125(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Dante M., Mamsley P.;			
CC	Submitted (Oct-1996) to the EMBL/Genbank/DBJ databases.			
CC	-1- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TO			
CC	SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS (BY			
CC	SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY). ACCUMULATES IN THE			
CC	ENDOPASMIC RETICULUM.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY BUT DIFFERENTIALLY IN A			
CC	VARIETY OF NEURAL AND NONNEURAL TISSUES.			
CC	-1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 SEMA DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	-----			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; U28369; AAD09138.1; -			
DR	EMBL; U73167; AAC02731.1; -			
DR	Genew; HGNC:10724; SEMA3B.			
DR	MIM; 601281; -			
DR	InterPro; IPR003559; IG.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003659; Plexin-like.			
DR	InterPro; IPR001627; Sema.			
DR	Pfam; PF00047; Ig; 1.			
DR	Pfam; PF01403; Sema; 1.			
DR	SMART; SM00409; IG; 1.			
DR	SMART; SM00423; PSI; 1.			
DR	Signal; Immunoglobulin domain; Multigene family; Glycoprotein.			
FT	CHAIN	1	24	POTENTIAL.
FT	CHAIN	25	749	SEMAPHORIN 3B.
FT	DOMAIN	239	537	SEMA.
FT	DOMAIN	637	717	IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	699	702	POLY-GLY.
FT	DOMAIN	724	744	ARG-RICH (BASIC).
FT	DISULFID	644	710	BY SIMILARITY.
FT	CARBOHYD	82	82	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	124	124	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	427	427	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	29	36	PRLSTO --> HAFGSPSK (IN REF. 2).
FO	SEQUENCE	749 AA;	83121 MW;	1F3BBF63F9444AF3 CRC64;

Query Match Similarity 17.4%; Score 368; DB 1; Length 749;  
Best Local Similarity 28.9%; Pred.No.1,7e-23;  
Matches 127; Conservative 49; Mismatches 167; Indels 96; Gaps 18;

CC

DB 7 GRAAASAPARVALSIPARFGLPLRLLLVFWVAASAAGHSGSPRISAVAKGDHYDF 66  
| | | | |  
+ + + + +

OY 22 GSAAASPPRLRL-----STQELQA-WHGIDTFSL 49  
+ + + + +

OY 67 SQPEPHVLVEHPGSESWVGKGVYHFNFPEGKNASYRTVN-----G 111  
+ + + + +

DB 50 ERTCCYQALLVDEEGRFLTVGAENNVASLNT--DNISKRAKKIAMPAPVEMREECNMAG 106  
+ + + + +

OY 112 SRKSGCQDKQDCGNITTLER-RGNGILVCGNNARKPSC-----NLVNDVSVM-----SL 161  
+ + + + +

DB 107 KDIGT-----ECOMNIVKLIHAVNRTHILLACGGAHNPICAFAYEGVGHRAEEPLRDPCRI 161  
+ + + + +

OY 162 GEMKYAEFPSPDENSLVLEEGDEVYSTIRKOYEYNGKIPFRIRIGESELTYT---SDTWQ 218  
+ + + + +

DB 162 EDGKRKSPTDPHRNAASVLYGEELLTSGVAADLMGDDFTIFRSLGQRPSLTRPHDSRWLN 221  
+ + + + +

OY 219 NFOPIKA-TYHQDQAYDDKIYFFREDNPDKNPE-APLNSRVALOCRGDGGSSELSV 276  
+ + + + +

DB 222 BEKFVKVWIPESENPDDDKIYFFPRETAVEAAPALGRLSVRGQICRNDGQORSL-V 280  
+ + + + +

OY 277 SKWNFIKLAMIVCS--DAATNENFRLODYVELLPDPSGGMROTTRYGVFSNP---WNNSA 331  
+ + + + +

DB 281 NKMTFLFARLKCVSGVYGEDTHFDOLDVFLL--SSRDHRPLLTYAVFTSSSIYFGSA 338  
+ + + + +

OY 332 VCVYSVLGDIIDRYF-----RTSLKGHYHGLSNPRPGMCLPKK-----OPIPT 374  
+ + + + +

DB 339 VCVYSMDVVRARFLCPFAHKESPMHWWSYQGRVYVYPARGKC-PKTIOTCTFSSTDFDD 397  
+ + + + +

OY 375 TFQVADSHPEVAQAVEPMG 393  
+ + + + +

DB 398 VIQFARNHPLMYNSVLPTG 416  
+ + + + +

RESULT 5  
SM3A\_HUMAN STANDARD; PRT; 771 AA.  
ID SM3A\_HUMAN Q14563;  
AC 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Semaphorin 3A precursor (Semaphorin III) (Sema III).  
NM Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal brain;  
RX MEDLINE=94094332; Pubmed-8269517;  
RT Kolodkin A.L., Matthes D.J., Goodman C.S.;  
RT "The semaphorin genes encode a family of transmembrane and secreted  
growth cone guidance molecules.";  
RT Cell 75:1389-1399(1993).  
RN [2]  
RP SEQUENCE OF 1-37 FROM N.A.  
RC Woessner J., Minx P., Hinds K., Strommatt C.;  
RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 39-182 FROM N.A.  
RC Rohlfing T., Tin-Wollam A.M., Duckels G.;  
RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL GROWTH  
CONES. COULD SERVE AS A LIGAND THAT GUIDES SPECIFIC GROWTH CONES  
BY A MOTILITY-INHIBITING MECHANISM. BINDS TO THE COMPLEX  
NEUROPLIN-1/PLEXIN-1 (BY SIMILARITY).  
CC -! SUBCELLULAR LOCATION: Secreted (by similarity).  
CC -! DOMAIN: STRONG BINDING TO NEUROPLIN IS MEDIATED BY THE CARBOXY  
TERMINUS OF THE PROTEIN.

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CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
CC -1- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L26081; AAA65938.1; -
CC EMBL: AC004451; AAC06185.1; -
CC EMBL: AC004848; AAC78622.1; -
CC Genew: HGNC:10723; SEMA3A.
CC MIM: 603961; -
CC InterPro: IPR003599; Ig.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003659; Plexin-like.
CC InterPro: IPR001627; Sema.
CC Pfam: PF00047; Ig; 1.
CC Pfam: PF01403; Sema; 1.
CC SMART: SM00409; IG; 1.
CC SMART: SM00423; PSI; 1.
CC Signal: Immunoglobulin domain; Multigene family; Neurogenesis;
CC Developmental protein; Glycoprotein.
CC SIGNAL: 1 20
CC CHAIN: 21 771
CC DOMAIN: 240 538
CC DOMAIN: 642 729
CC DOMAIN: 727 769
CC DISULFID: 649 722
CC CARBOHYD: 53 53
CC CARBOHYD: 125 125
CC CARBOHYD: 590 590
CC SEQUENCE: 771 AA; 88889 MW; 9985F8D3EAED8456 CRC64;

Query Match      17.1%; Score 363; DB 1; Length 771;
Best Local Similarity 28.0%; Pred. No. 4.8e-23;
Matches 119; Conservative 66; Mismatches 162; Indels 78; Gaps 19;

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RESULT 6
ID SM3B_MOUSE STANDARD; PRT; 748 AA.
AC 062177;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Semaphorin 3B precursor (Semaphorin A) (Sema A).
GN SEMA3B OR SEMA OR SEMA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Embryo;
RX MEDLINE=95267431; PubMed=7748561;
RA Puschel A.W., Adams R.H., Betz H.;
RT "Murine semaphorin D/collapsin is a member of a diverse gene family
RL and creates domains inhibitory for axonal extension.";
RL Neuron 14:941-948(1995).
CC -1- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TO
CC SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED FROM DAY 10 IN THE EMBRYO. LOW
CC LEVELS FOUND BETWEEN DAYS 10-12. EXPRESSION PEAKS ON DAY 13 WITH
CC MODERATE LEVELS FROM THEN UNTIL BIRTH.
CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
CC -1- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X85990; CAA59982.1; -
CC MGD: MGI:107561; Sema3b.
CC InterPro: IPR003599; Ig.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003659; Plexin-like.
CC Pfam: PF00047; Ig; 1.
CC Pfam: PF01403; Sema; 1.
CC SMART: SM00409; IG; 1.
CC SMART: SM00423; PSI; 1.
CC Signal: Immunoglobulin domain; Multigene family; Neurogenesis;
CC Developmental protein; Glycoprotein.
CC SIGNAL: 1 25
CC CHAIN: 26 748
CC DOMAIN: 239 536
CC DOMAIN: 636 716
CC DOMAIN: 698 732
CC DOMAIN: 723 743
CC DISULFID: 643 709
CC CARBOHYD: 82 82
CC CARBOHYD: 124 124
CC SEQUENCE: 748 AA; 82894 MW; 1866B7D2397C9305 CRC64;

Query Match      17.1%; Score 361.5; DB 1; Length 748;
Best Local Similarity 29.9%; Pred. No. 6.1e-23;
Matches 133; Conservative 51; Mismatches 152; Indels 109; Gaps 23;

```

Db	82	NISKRAKKLA--W-----PAPVEMRECN--MAG-----	106
Qy	106	RTVINGSTRKSGQDQDQDQDQNTYTLLERRN-GLVYCGTAAKRPSC-----WNLVNDSVMS	160
Db	107	--KDIGT-----ECNNFVRLHAAVHTHLACRTAEPHTCGLMWATAGGTHAST	155
Qy	161	----GEMKGYAPFSPDENSLVLFEGDEVEYSTRKOEYNGKIPRFRRIGSESLY- 156 GPEKLEDDCKGKPYDPRIHRPSPVLVIGELYSQVTDADMGRDPTIFPSLQONSRLTEPHD	215
Qy	214	DTVMNQPFICA-TVHODADVDKIYFFREDNPDKNE-APLNVSRVAQLCRGDQGE	271
Db	216	SRMLPEPFVKKFWMPESENPDDDKTYFFRESAVEAAPAMGRMSYSRVGOICRNDLGO	275
Qy	272	SLSVSKNNFTLAKALVCS--DAATNRNPNRIADVFLLDPDPSGQMDT--RYVGVSFSP--	326
Db	276	RSL-VNKKMTTFLAKALVCSVPGVEGDTHDDQLDQVFL--SSRDQDTLLLAIVFTSSG	331
Qy	327	-WNSAVCVYSLGIDIRVF-----RTSSLKGYHMLSNPPRCMLPKK-----	368
Db	332	VEOGSAVCVYSNMNDVRAFLGLPFRKEGPTHQWMSYOGRVYPYPRDQC-PSKTFGTFSST	390
Qy	369	QPIPEFEOVADSHPEVAQRPVPMG 393	
Db	391	KDFPDVIOGFRNHPLMTNPVPLMG 415	
RESULT 7			
SM4D_HUMAN	ID	SM4D_HUMAN	STANDARD: PRT: 862 AA.
AC	Q92854		
DT	30-MAY-2000	(Rel. 39, Created)	
DT	30-MAY-2000	(Rel. 39, Last sequence update)	
DT	16-OCT-2001	(Rel. 40, Last annotation update)	
DE	Semaphorin 4D precursor (Leukocyte activation antigen CD100) (BB18)		
DE	(AB) (GR3)		
GN	SEMAPD OR CD100.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_Taxid:9606;		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-T-cell;		
RX	MEDLINE-97030273; PubMed-8876214;		
RA	Hall K.T., Boumsell L., Schultze J.L., Boussioutis V.A., Dorfman D.M.,		
RT	Cardoso A.A., Bensussan A., Nadler L.M., Freeman G.J.;		
RT	"Human CD100, a novel leukocyte semaphorin that promotes B-cell		
RT	regression and differentiation.";		
RT	Proc. Natl. Acad. Sci. U.S.A. 93:11780-11785(1996).		
CC	-1- FUNCTION: MAY PLAY A FUNCTIONAL ROLE IN THE IMMUNE SYSTEM, AS WELL		
CC	AS IN THE NERVOUS SYSTEM. INDUCES B CELLS TO AGGREGATE AND		
CC	IMPROVES THEIR VIABILITY IN VITRO.		
CC	-1- SUBUNIT: HOMODIMER.		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL MUSCLE,		
CC	PERIPHERAL BLOOD LYMPHOCYTES, SPLEEN, AND THYMUS AND ALSO		
CC	EXPRESSED AT LOWER LEVELS IN TESTES, BRAIN, KIDNEY, SMALL		
CC	INTESTINE, PROSTATE, HEART, PLACENTA, LUNG, AND PANCREAS BUT NOT		
CC	IN COLON OR LIVER.		
CC	-1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.		
CC	-1- SIMILARITY: CONTAINS 1 SEVA DOMAIN.		
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.		
CC	-1- DATABASE: NAME=PROV; NOTE=CD CD100 entry;		
CC	WWW="http://www.ncbi.nlm.nih.gov/ptow/cd/cd100.htm".		
CC	-----		
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[illegible]

RESULT 8  
 SM3A\_MOUSE STANDARD: PRT: 772 AA.  
 AC 008665: 062180: 062215:  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Semaphorin 3A precursor (Semaphorin III) (Sema III) (Semaphorin D) (Sema D)  
 GN SEMA3A OR SEMAD OR SEMD.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NMRI; TISSUE=Embryo;  
 RX MEDLINE=95267431; PubMed=7748561;  
 RA Puschel A.W., Adams R.H., Betz H.;  
 RT "Murine semaphorin D/collapsin is a member of a diverse gene family  
 RT and creates domains inhibitory for axonal extension.";  
 RL Neuron 14:941-946(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97470885; PubMed=9331345;  
 RA Taniguchi M., Yusa S., Fujisawa H., Naruse I., Saga S., Mishina M.,  
 RA Yagi T.;  
 RT "Disruption of semaphorin III/D gene causes severe abnormality in  
 RT peripheral nerve projection.";  
 RL Neuron 19:519-530(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Kimura T., Fishman M.C.;  
 RT "CDNA sequence of mouse collapsin/semaphorin III.";  
 RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 107-772 FROM N.A.  
 RC TISSUE=Fetal brain;  
 RX MEDLINE=95267432; PubMed=7748562;  
 RA Messersmith E.K., Leonardo E.D., Shatz C.J., Tessier-Lavigne M.,  
 RA Goodman C.S., Kolodkin A.L.;  
 RT "Semaphorin III can function as a selective chemorepellent to pattern  
 RT sensory projections in the spinal cord.";  
 RL Neuron 14:949-959(1995).  
 CC - FUNCTION: PLAY A ROLE IN GROWTH CONES GUIDANCE. MAY FUNCTION TO  
 CC PATTERN SENSORY PROJECTIONS BY SELECTIVELY REPELLING AXONS THAT  
 CC NORMALLY TERMINATE DORSALLY.  
 CC - SUBCELLULAR LOCATION: Secreted.  
 CC - DEVELOPMENTAL STAGE: EXPRESSED EARLY IN EMBRYONIC DEVELOPMENT  
 CC (E11) IN DISTINCT REGIONS OF THE NEUROECTODERM AND MESODERM.  
 CC EXPRESSION BECAME MORE EXTENSIVE AT LATER STAGES.  
 CC - DOMAIN: STRONG BINDING TO NEUROPILIN IS MEDIATED BY THE CARBOXY  
 CC THIRD OF THE PROTEIN.  
 CC - SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.  
 CC - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
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 CC  
 CC EMBL: X85993; CAA59985.1; -  
 CC EMBL: D85028; BAA19773.1; -  
 CC EMBL: L41541; AAL77611.1; -  
 CC EMBL: L40484; AAA73934.1; -  
 CC MGD: MGI:107558; Sema3a.  
 CC InterPro: IPR003599; Ig.  
 CC InterPro: IPR003006; Ig\_MHC.  
 CC InterPro: IPR003659; Plexin-like.

DR InterPro: IPR001627; Sema.  
 DR Pfam: PF00047; Ig.1.  
 DR Pfam: PF01403; Sema; 1.  
 DR SMART: SM00409; Ig; 1.  
 DR SMART: SM00423; PSI; 1.  
 KW Signal: Immunoglobulin domain; Multigene family; Neurogenesis;  
 KW Developmental protein; Glycoprotein.  
 FT SIGNAL 1 20  
 FT CHAIN 21 772  
 FT DOMAIN 240 538  
 FT DOMAIN 643 730  
 FT DOMAIN 728 772  
 FT DISULFID 650 723  
 FT CARBOHYD 53 53  
 FT CARBOHYD 125 125  
 FT CARBOHYD 591 591  
 FT CONFLICT 193 193  
 FT CONFLICT 207 207  
 FT CONFLICT 253 253  
 FT CONFLICT 352 352  
 FT CONFLICT 403 403  
 FT CONFLICT 571 572  
 FT CONFLICT 616 620  
 FT CONFLICT 623 623  
 SQ SEQUENCE 772 AA; 88799 MW; E89A08528B10AEC3 CRC64;  
 Query Match 16.9%; Score 359; DB 1; Length 772;  
 Best Local Similarity 28.3%; Pred. No. 1e-22;  
 Matches 119; Conservative 62; Mismatches 163; Indels 76; Gaps 19;  
 QY 36 VFWVAASAGSHRSRSG---PRISAVWK-----GQDHVDF-----SQEPHTVFEHSGSFS 83  
 DB 10 LFWGVLLTRANRYANGKNNVPRKLKSYKEMLESNNVITFNGLANSSYTFLLDERS- R 68  
 QY 84 VVWGSGKYYHNPFGKNAVSRTVNGSTKSCODK-----QDCGNYITLLER- R 133  
 DB 69 LVYGAADHIFSPNLVNIKQFOKIWVVSYTR--RDECKWAGKDLKECANFIKYLEAVN 125  
 QY 134 GNGLVCCGNNAKRPSCWNL-----VNDYSVMSLGEMKGYAPSPDBNSLVLE 181  
 DB 126 QTHLYACGAGRHPICTYLEVGHNEPDNIFKLQDS---HFENGKSPYDPKLLTPASLDI 182  
 QY 182 GDEVSTIRKQZYNKGIPIFRRIKGESELYT---SPTVQNPQFIRKATV-HQDAVYDK 237  
 DB 183 DSELVSGTRADMGDFALFRTLGHHNPIRTQHDHSMKLNDRFSAHLIPSDNEPDK 242  
 QY 238 IYFFREDNPDKNPEAPLNVSRVAQLCRGDGSGESSLVSKNNTFLKAMLYCSDAATN-- 295  
 DB 243 VVEFFRENALIDGHSKATNARIQCKNDPFGHRL-VNKKTTFLKARLICSVPENGI 301  
 QY 296 -RNEFRLOVFL--PDPSGQMRDTRVYGVF---SNPMYSAVCYVSLGDDIRVF----- 344  
 DB 302 DTHFDLOVFLMNSKDP---KNPIYGVFTTSSNIFGSAVCMYSMSDVRVFLGPYA 357  
 QY 345 -----RTSSLKGYHMGLSNRPQGLPKK-----QPIPTENFYQVADSHPEVQAQVEPM 392  
 DB 358 HNDGPNYQWNPYQGRVPRPRGTC-PSKITFGGFDSTKLDLDDVITFARSHPAIYNVFPPI 416  
 RESULT 9  
 SM4B\_MOUSE STANDARD: PRT: 782 AA.  
 AC 062179:  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Semaphorin 4B (Semaphorin C) (Sema C) (Fragment).  
 GN SEMA4B OR SEMAC OR SEMC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]



RP SEQUENCE FROM N.A.  
RC STRAIN-NMRT; TISSUE=Brain;  
RA MEDLINE=95267431; PubMed=7748561;  
RA Pueschel A.W., Adams R.H., Betz H.;  
RT "Murine semaphorin D/collapsin is a member of a diverse gene family  
RT and creates domains inhibitory for axonal extension.";  
RL Neuron 14:941-948(1995).  
RN [2]  
RP INTERACTION WITH GIPC.  
RX MEDLINE=99253973; PubMed=10318831;  
RA Wang L.-H., Kalb R.G., Strittmatter S.M.;  
RT "A PDZ protein regulates the distribution of the transmembrane  
RT semaphorin, M-SemF".  
RL J. Biol. Chem. 274:14137-14146(1999).  
CC -1- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TO  
CC SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS.  
CC -1- SUBUNIT: INTERACTS WITH GIPC PDZ DOMAIN.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED FROM DAY 10 IN THE EMBRYO. LOW  
CC LEVELS FOUND BETWEEN DAYS 10-12. EXPRESSION PEAKS ON DAY 13 WITH  
CC MODERATE LEVELS FROM THEN UNTIL BIRTH.  
CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 SEMA DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
CC -----  
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CC -----  
CC EMBL; X85992; CAA59984.1; -  
DR MGD; MGI:107559; Sema4b.  
DR InterPro: IPR003659; Plexin-like.  
DR InterPro: IPR002165; Plexin\_repeat.  
DR InterPro: IPR001627; Sema.  
DR Pfam; PF01403; Sema; 1.  
DR Pfam; PF01437; PSI; 1.  
DR SMART; SM00423; PSI; 1.  
KW Transmembrane; Immunoglobulin domain; Multigene family; Neurogenesis;  
KW developmental protein; Glycoprotein.  
FT NON\_TER 1  
FT DOMAIN 1 662  
FT TRANSMEM 663 683 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 684 782 POTENTIAL.  
FT DOMAIN 202 492 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 548 608 SEMA.  
FT DOMAIN 703 726 IG-LIKE C2-TYPE DOMAIN.  
FT DISULFD 555 601 PRO-RICH.  
FT CARBOHYD 12 12 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 526 526 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 782 AA; 86823 MW; 627A81FEC9F87AC8 CRC64;  
Query Match 16.8%; Score 355.5; DB 1; Length 782;  
Best Local Similarity 31.0%; Pred. No. 2,1e-22;  
Matches 104; Conservative 47; Mismatches 138; Indels 47; Gaps 14;  
OY 72 HTVLFHEGSGSVWVGKGYHFN-----PPEGKASVRYVNIQSTGSC-----QDKQ 121  
DB 16 YTALLSDQGTGLTYGAREALFALMSNLSPFLGGEYDELLMSADADRRKQCGFKGDKPKR 75  
OY 122 DCGNFI-TLLEBRGGLLVCGNNARKPSC-----NMLVND-----SVNMSGEMKGAPE 170  
DB 76 DCQNTIKTLPLINSCHLLTGCIAVSPICAYIHIASTFLADQAGNVLLDEG--KGHCPE 133

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QY 171 SPDENSLVFEDEBYSTIRKROEYGNCKIPRFRRIERGESELIYTSQV--MOMPOKIAIV 228
Db 134 DENKSTALVVDGELY-TGYVSSFGQNDPAISRSOSSRPRTYESSLNMLDPAFVASYTS 192
QY 229 HODQAV----DKIYVFFEREDNPDKNPEAPLVNSVVAOLCRDQDGSSELSYSKWNFLK 284
Db 193 PSLSLSPIGDDDKIYFFSFETQGEFFENFTLVSNVAIVCKGDEGEAVLQ-QHRTSLK 251
QY 285 AMLVCSDAATNENFRLODVELL-PDPSGQMQRDTRVYVFSFNPNY-----SAYCVSLG 338
Db 252 AQLLSRPDDGPFPEVLVDVFTLNPNO-DWKKTLSTLIVFTSQMHRGTTEGSAICVFTMN 310
QY 339 DIDRVF-----RTSLKGYHMGSLNPRGMCL 365
Db 311 DVQKAFDGLYKKVNRETOQWYTHQVPTPRGACT 346

RESULT 10
SM3A_RAT
ID SM3A_RAT STANDARD: PRT: 772 AA.
AC 063548:
DF 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DR 16-OCT-2001 (Rel. 40, Last annotation update)
DE Semaphorin 3A precursor (Semaphorin III) (Sema III).
GN SEMA3A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP
RT SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=97073089; PubMed=8915837;
RA Giger R.J., Wolter D.P., De Wit G.M.J., Verhaagen J.;
RT "Anatomy of rat semaphorin Iii/collapsin-1 mRNA expression and
RT relationship to developing nerve tracts during neuroembryogenesis.";
RL J. Comp. Neurol. 375:378-392(1996).
CC -FUNCTION: MAY BE INVOLVED IN GUIDING GROWING AXONS TOWARDS THEIR
CC TARGETS BY FORMING A MOLECULAR BOUNDARY THAT INSTRUCTS AXONS TO
CC ENGAGE IN THE FORMATION OF SPECIFIC NERVE TRACTS. BINDS TO
CC NEUROFILIN.
CC -SUBCELLULAR LOCATION: Secreted (By similarity).
CC -DEVELOPMENTAL STAGE: At E-11, EXPRESSION WAS RESTRICTED TO THE
CC OLFACTORY PIT, THE BASAL AND ROSTRAL SURFACE OF THE TELENEPHALIC
CC VESICLE, THE EYE ANLAGE, THE EPITHELIUM OF RATHKE'S POUCH, AND
CC SOMITES. AT LATER DEVELOPMENTAL STAGES, IT WAS WIDELY DISTRIBUTED
CC IN NEURONAL AS WELL AS IN MESENCHYMAL AND EPITHELIAL STRUCTURES
CC OUTSIDE THE NERVOUS SYSTEM. AFTER BIRTH, MESENCHYMAL LEVELS
CC DECREASED RAPIDLY AND EXPRESSION BECAME RESTRICTED TO SPECIFIC
CC SEFS OF NEURONS IN THE CNS. IN THE MATURE CNS, IT IS DETECTABLE IN
CC MITRAL CELLS, NEURONS OF THE ACCESSORY BULB AND CEREBRAL CORTEX,
CC CEREBELLAR PURKINJE CELLS, AS WELL AS A SUBSET OF CRANIAL AND
CC SPINAL MOTONEURONS.
CC -DOMAIN: STRONG BINDING TO NEUROFILIN IS MEDIATED BY THE CARBOXY
CC THIRD OF THE PROTEIN.
CC -SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
CC -SIMILARITY: CONTAINS 1 SEMA DOMAIN.
CC -SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -----
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CC -----
DR EMBL: X95286; CAAG64607.1; -.
DR InterPro: IPR0003599; Iq.
DR InterPro: IPR0003506; Iq_MHC.
DR InterPro: IPR0003659; Plexin-like.
DR

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DR InterPro: IPR001627; Sema.  
 DR Pfam: PF00047; Ig. 1.  
 DR SMART: SM00403; Sema. 1.  
 DR SMART: SM00409; Ig. 1.  
 DR SMART: SM00423; PSI. 1.  
 DR Signal: Immunoglobulin domain; Multigene family; Neurogenesis;  
 KW Developmental protein; Glycoprotein.  
 FT SIGNAL 1 20  
 FT CHAIN 21 772 SEMAPHORIN 3A.  
 FT DOMAIN 240 538 SEMA.  
 FT DOMAIN 643 730 IG-LIKE C2-TYPE DOMAIN.  
 FT DOMAIN 728 770 ARG/LYS-RICH (BASIC).  
 FT DISULFID 650 723 BY SIMILARITY.  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 772 AA; 88808 MW; 240907812FF9E2D2 CRC64;  
 Query Match 16.7%; Score 354; DB 1; Length 772;  
 Best Local Similarity 28.1%; Pred. No. 2,8e-22;  
 Matches 118; Conservative 63; Mismatches 163; Indels 76; Gaps 19;  
 QY 36 VFWVAASAQGHRSRG---PRISAVMK---GQDHVDF---SQEPHTVLFHEPGSFS 83  
 DB 10 LFWGILLTARANYANGKNVPRKLKLYKEMLESNNVITFENGLANSSYHTFLDEERS-R 68  
 QY 84 VVWVGGRGVYHFNPECKNASVRYNIGSTKSCODK-----QDCGNITLLER-R 133  
 DB 69 LVVGAKKDHFEFNLVNIKDFOKIWPVSYTR--RDECKWACKDLKECANFIKYLKAVN 125  
 QY 134 GNGLLVCGTNAKPPSCWNL-----VNDSEVMSLGEKMGYAPSPDENSLVLE 181  
 DB 126 QTHLYACGGAHFICTYIEVGHHPEDNIFKLDS---HFENGGRKSPYDPLILASILLI 182  
 QY 162 GDEVYSTRKOEYNGKIPFRRIKGESELYT--SDTVNQNQOFIKATIV-HQDAYDK 237  
 DB 183 DGLSYGTAADPMGDFALFTLGHNNPRTIQRHDSRWMLNDPRTISANHLIPESDNPEDDK 242  
 QY 238 IYFFREDNPCKNPPAPLVNSVVAOLCRDQGESLSKNTFLKALVCSDAATN-- 295  
 DB 243 VYFEFRENALIDESHGKATIHARIQICNDFFGHSRL-VNKKWTFLLKALISVPGNGI 301  
 QY 296 -RNFNRLQDVFL--PDPSGQWRDTRVYGVF--SNPMNYSAYVYSLCIDIRVF----- 344  
 DB 302 DTHFELQDVFLMNSKDP-----KNPIYGVFTTSSNIFFGSAVCMTSMKDVAVRFLGPA 357  
 QY 345 ---RTSSLKGYHMLSNRPDMCLPK-----QPIPTETFOVADSHPEVAQRVEM 392  
 DB 358 HRDGNVQWVYQGRVYPRPGTC-PSKTFGGFDSFKDLDPDVTIFARSHPMYNPVPEI 416  
 RESULT 11  
 SM3A\_CHICK STANDARD: PRT; 772 AA.  
 ID SM3A\_CHICK Q90607;  
 AC Q90607;  
 DT 30-MAY-2000 (Rel. 39, last sequence update)  
 DT 30-MAY-2000 (Rel. 39, last sequence update)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE Semaphorin 3A precursor (Collapsin-1) (COLL-1).  
 GN SEMA3A OR COL1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 322-329; 362-372; 395-403 AND 666-680.  
 RC TISSUE=Brain;  
 RX MEDLINE=94006554; PubMed=8402908;  
 RA Luo Y., Rabile D., Raper J.A.;  
 RT "Collapsin: a protein in brain that induces the collapse and paralysis of neuronal growth cones.";

RL Cell 75:217-227(1993).  
 CC -I- FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL GROWTH  
 CC CONES. COULD SERVE AS A LIGAND THAT GUIDES SPECIFIC GROWTH CONES  
 CC BY A MOTILITY-INHIBITING MECHANISM. BINDS TO NEUROPILIN.  
 CC -I- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -I- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN BRAIN  
 CC AND MUSCLE. MODERATE LEVELS IN LUNG, BURSAS, AND HEART AND  
 CC VIRTUALLY ABSENT IN LIVER. COLLAPASIN-1, -2, -3, AND -5 BIND TO  
 CC OVERLAPPING BUT DISTINCT AXON TRACTS.  
 CC -I- DOMAIN: STRONG BINDING TO NEUROPILIN IS MEDIATED BY THE CARBOXY  
 CC THIRD OF THE PROTEIN.  
 CC -I- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.  
 CC -I- SIMILARITY: CONTAINS 1 SEMA DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL: U02528; AAC59638.1; -;  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003606; Ig.MHC.  
 DR InterPro: IPR003659; Plexin-like.  
 DR InterPro: IPR001627; Sema.  
 DR Pfam: PF00047; Ig. 1.  
 DR Pfam: PF00403; Sema. 1.  
 DR SMART: SM00409; Ig. 1.  
 DR SMART: SM00423; PSI. 1.  
 DR Signal: Immunoglobulin domain; Multigene family; Neurogenesis;  
 KW Developmental protein; Glycoprotein.  
 FT SIGNAL 1 22  
 FT CHAIN 23 772 SEMAPHORIN 3A.  
 FT DOMAIN 240 538 SEMA.  
 FT DOMAIN 643 730 IG-LIKE C2-TYPE DOMAIN.  
 FT DOMAIN 728 770 ARG/LYS-RICH (BASIC).  
 FT DISULFID 650 723 BY SIMILARITY.  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 772 AA; 88867 MW; E91E09DE0CC940AC CRC64;  
 Query Match 16.5%; Score 350; DB 1; Length 772;  
 Best Local Similarity 28.6%; Pred. No. 6.1e-22;  
 Matches 123; Conservative 56; Mismatches 165; Indels 86; Gaps 19;  
 QY 29 LRLRLILVFWVAASAQGHRSRGPRISAVMK---GQDHVDF---SQEPHTVLFHEPG 80  
 DB 7 IALLSLGVLLAGRVNQHKNVPRKLKLYKEMLESNNVITFENGLANSSYHTFLDEER 66  
 QY 81 SFSVWVGGRGVYHFNPECKNASVRYNI-----GSTKSCQ-----DKQDCG 124  
 DB 67 S-RLVYAGKADHIFSL-----VNIKEYQKIWPVSHSRDECKWACKDLIRECA 115  
 QY 125 NYITLLER-RGNGLLVCGTNAKPPSCWNL-----VNDSEVMSLGEKMGYAPSP 171  
 DB 116 NFIKVLKTYNQTHLYACGGAHFPMCTYIEVSHPEDNIFRMDSS--HFENGGRKSPYD 172  
 QY 172 PDENSLVLEGEDEVYSTRKOEYNGKIPFRRIKGESELYT--SDTVNQNQOFIKATIV 228  
 DB 173 PKLLTASLVLDELQVSGTADEPMGDFALFTLGHNNPRTIQRHDSRWMLNDPRTISANHLI 232  
 QY 229 -HQDAYDKIYFFREDNPCKNPPAPLVNSVVAOLCRDQGESLSVSKNTFLKAML 287  
 DB 233 PDSNDNEDDKIYFFRENALIDESHGKATIHARIQICNDFFGHSRL-VNKKWTFLLKAL 291  
 QY 288 VCSDAATN--RNFNRLQDVFL--PDPSGQWRDTRVYGVF--SNPMNYSAYVYSLCID 339  
 DB 292 ICSVPNGIDITHFELQDVFLMNSKDP-----KNPIYGVFTTSSNIFFGSAVCMTSM 347

QY 340 IDRVF-----RTSSLKGYHMGSLNPRQMCIPRK-----QPIPTETFOVADSH 382  
 DB 348 VRRFLGAYHARDGPNYQWVYQGRVYPRPGTGC-PSKTFGPGDSTKDLDPDEVITFAKSH 406  
 QY 383 PEVAQREPEM 392  
 DB 407 PAMYNVFPFI 416

## RESULT 12

SZLA\_BRAE STANDARD: PRT: 860 AA.  
 ID SZLA\_BRAE  
 AC Q9W7J1;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Semaphorin 21A precursor (Semaphorin 1A) (Sema-21A).  
 GN SEMAZ1A OR SEMAZ1A.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_Taxid=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Embryo;  
 RX MEDLINE=99313409; PubMed=1036838;  
 RA Yee C.S., Chandrasekhar A., Halloran M.C., Shoji W., Warren J.T.,  
 RA Kuwada J.Y.;  
 RT "Molecular cloning, expression, and activity of zebrafish semaphorin 21A."  
 RL Brain Res. Bull. 48:581-593(1999).  
 CC -FUNCTION: MAY INFLUENCE OUTGROWTH BY A VARIETY OF GROWTH CONES  
 CC INCLUDING THOSE OF THE POSTERIOR LATERAL LINE GANGLION.  
 CC -SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -DEVELOPMENTAL STAGE: EXPRESSED IN HIGHLY SPECIFIC PATTERNS WITHIN  
 CC THE DEVELOPING EMBRYO.  
 CC -SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.  
 CC -SIMILARITY: CONTAINS 1 SEMA DOMAIN.  
 CC -SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF086761; AAD43964.1;  
 DR ZFIN: ZDB-GENE-991209-3; semaz1a.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003659; Plexin-like.  
 DR InterPro: IPR001627; Sema.  
 DR Pfam: PF00047; Ig\_1.  
 DR Pfam: PF01403; Sema; 1.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00423; PST; 1.  
 KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;  
 KW Developmental protein; Glycoprotein.  
 FT CHAIN 1  
 FT SIGNAL 1  
 FT CHAIN 18 860  
 FT DOMAIN 241 539  
 FT DOMAIN 645 724  
 FT DOMAIN 722 858  
 FT DOMAIN 652 717  
 FT DISULFID 53 53  
 FT CARBOHYD 53 53  
 FT CARBOHYD 126 126  
 FT CARBOHYD 593 593  
 SO SEQUENCE 860 AA; 97263 MW; 5FDAC12194F5165C CRC64;  
 Query Match 16.5%; Score 349; DB 1; Length 860;

Best Local Similarity 26.6%; Pred. No. 8.6e-22;  
 Matches 122; Conservative 55; Mismatches 155; Indels 126; Gaps 21;

QY 6 PGRAPASAPRARVLSLPARFGILRLRLLLVFWMAAASQHS---RSGPRISAQWKOD 62  
 DB 17 PGRVAPQHTKKEVLPRLKLSYNEMLSSNLVTF-TGLANSSGVDPLMDGERGLLVGAE 75  
 QY 63 HVDFSQPEPHVTLFHEPQSFVWVGKGVYHFNPEPEGKNASVFTVNG----- 111  
 DB 76 HV-----FSFD-----LVNINROVKQIAMPAT 97  
 QY 112 -STGSCQ-----DKDCGNVITLLER-RGNGLVCGTNARKPSCWNLVDSVWVSLGEM 164  
 DB 98 PSKRDECKWACKDLRKDCNSFVRLQSYNQHIIYICGTGAFHPIC-----SPEEMGKR 150  
 QY 165 -----KQAPFSPDENSELVFEDEGEVSTIRKQEVNKKIRPRIRRES 208  
 DB 151 AEDNIFRLDANYFENGRRKSPYDPKMQSSLLLDGELYSGSADPMGRDFAIFRLGSHH 210  
 QY 209 ELYT---SDIWMONPOFIKATIV-HQDAYDDKIYFFREDNPPKNEPAPLNVSRVQLC 264  
 DB 211 PIRTEQHDSRWLNPRFLGILHILPESDNPEDDKIFLFFKENAMQCEHTGKATISRIQLC 270  
 QY 265 RGDOGESSLSVSKWNTFLKAMLVCSDAATN---RNFRLQDVLL--PDPSGQWRDTRV 319  
 DB 271 KNDMGHRSR-VNKRWTFELKAKITCSVPGGLNGIDITHPELDQVFLMSAKDP-----KNFVI 325  
 QY 320 YGVF---SNPNVSAVCYSLGDDIDRVFRTSSLAGY-HMGLSN-----PRPGM 363  
 DB 326 YAVFTTSSNIFRGSALICVSMADIRRVF---LQPYARDGPNYQWVYQGRVYPRPGT 381  
 QY 364 CLPKK-----QPIPTETFOVADSHPEVAQREPEM 393  
 DB 382 C-PSKTFGPGDSTKDLDPDVTFFRLHPRAMPYQPMG 418

## RESULT 13

SZM7\_BRAE STANDARD: PRT: 766 AA.  
 ID SZM7\_BRAE  
 AC Q9YHX4;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Semaphorin 27 precursor (Semaphorin 7) (Sema-27).  
 GN SEMAZ7 OR SEMA7.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_Taxid=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99060909; PubMed=9867349;  
 RA Halloran M.C., Severance S.M., Yee C.S., Gemza D.L., Kuwada J.Y.;  
 RT "Molecular cloning and expression of two novel zebrafish  
 RT semaphorins."  
 RL Mech. Dev. 76:165-168(1998).  
 CC -SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.  
 CC -SIMILARITY: CONTAINS 1 SEMA DOMAIN.  
 CC -SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL: AF073389; AAC72345.1;  
 DR ZFIN: ZDB-GENE-990715-7; sema7.  
 DR InterPro: IPR003006; Ig\_MHC.

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DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR002165; Plexin-repeat.
DR InterPro: IPR001627; Sema.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF01403; Sema; 1.
DR Pfam: PF01437; PSI; 1.
DR SMART: SM00410; Ig-like; 1.
DR SMART: SM00423; PSI; 1.
KW Signal; Transmembrane; Immunoglobulin domain; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 766 SEMAPHORIN 27.
FT DOMAIN 25 664 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 665 685 POTENTIAL.
FT DOMAIN 686 766 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 232 522 Sema.
FT DOMAIN 570 630 Ig-like C2-type domain.
FT DISULFID 577 623 BY SIMILARITY.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 766 AA; 85617 MW; 0ACBC693FE7D830C CRC64;

Query Match 16.2%; Score 344.5; DB 1; Length 766;
Best Local Similarity 29.8%; Pred. No. 1.8e-21;
Matches 114; Conservative 47; Mismatches 146; Indels 75; Gaps 18;

75 LHEPGSFVSVW-----VGGRGKYYHFNPE--GKNASVRTVNGSTGSGC 117
44 LFREEG---IWNVTMLRDDLRLILGAREALFALDLDITTKKMLKWEVARDQND 100
DB 118 QDK-----ODCGYITLLERRGNG-LLVCGTNARKSCWNLVDSVMSL-----GENKGY 167
DB 101 SNMGKDATNCKKNYIRILHKKNDGRMYVCCTKAFNPCCGLYADGKLTLEIILOEDTKGK 160
QY 168 APRSPD---NSLVLEGDEVYSTIRKQENKGIPIPRFRIRGES--ELYSDVVMQNPQF 222
DB 161 CPDPDPQRTSARV---DQATYSATSMNRSSEPMWMTRETESIRTEFS-TWLSPPNF 215
QY 223 IKATIWHODAY---DQKIYFFREDNPDKNEADPLNRSVAQLCGDGGESSLSVSK 278
DB 216 IHMAHLPREGOSNDGDDKIYLFSEFAVESEYTKVDSRVARVCKGLDGGQRTLO-KK 274
QY 279 WNTFLKAMLVCSDAATNRNENRLQDVF-LLDPGSGMRDTRVYGV---SNPMNYSAYCV 334
DB 275 WTSFLKARLDCCQVPNTNLP-LVQDVFHLCPP--DMTTCVFAYAVFTPOSDSSQYSAYCS 330
QY 335 YSLGIDIDRYEFTSSLKG-----YHMGLSNPRFGMC-----LPKKQPIR 372
DB 331 YKIEDIKTYFSKGRKFAFNVETSPFKWVWYSGELDPDRGACIDNHARKGKITKSLLEP 390
QY 373 TETFOYADSHPEVAORVEPMGP 394
DB 391 DKTLOEVKDKPLMDQAVTAEPQ 412

RESULT 14
S21B_BRARE STANDARD; PRT; 778 AA.
AC 09W686;
DT 30-MAY-2000 (Rel. 39, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Semaphorin 21B precursor (Semaphorin 1B) (Sema-21B).
GN SEMA21B OR SEMA3AB.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1].

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RP SEQUENCE FROM N.A.
RX MEDLINE-99425174; PubMed-10495275;
RA Roos M., Schachner M., Bernhardt R.R.;
RT "Zebrafish semaphorin 21b inhibits growing motor axons in vivo.";
RL Mech. Dev. 87:103-117(1999).
CC -1- FUNCTION: MIGHT NORMALLY INFLUENCE THE MIDSEGMENTAL PATHWAY CHOICE
CC OF THE VENTRALLY EXTENDING MOTOR AXONS BY CONTRIBUTING TO A
CC REPULSIVE DOMAIN IN THE POSTERIOR SOMITE.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN RHOMEROMERES THREE AND FIVE, AND
CC IN THE POSTERIOR HALF OF NEWLY FORMED SOMITES WHICH IS AVOIDED BY
CC VENTRALLY EXTENDING MOTOR AXONS.
CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
CC -1- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC
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CC or send an email to license@isb.slb.ch).
CC
CC EMBL: AF083382; AAD28103.1; -
CC ZFIN: ZDB-GENE-991209-6; sema3ab.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR002165; Plexin-repeat.
DR InterPro: IPR001627; Sema.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF01403; Sema; 1.
DR Pfam: PF01437; PSI; 1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00423; PSI; 1.
KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
KW Developmental protein; Glycoprotein.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 778 SEMAPHORIN 21B.
FT DOMAIN 241 539 SEMA.
FT DOMAIN 645 723 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 721 776 ARG/LYS-RICH (BASIC).
FT DISULFID 652 716 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 593 593 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 778 AA; 88904 MW; 4D36F4323AE21895 CRC64;

Query Match 16.2%; Score 342.5; DB 1; Length 778;
Best Local Similarity 28.8%; Pred. No. 2.7e-21;
Matches 124; Conservative 64; Mismatches 152; Indels 91; Gaps 25;

33 LLIVFWVAASAOG---HSRSG-PRISAVMK---GQDHVDF---SOEPHTVLFHEP 79
DB 7 IVLLIWLILAPRGCTVQNRKSKSNVRLKPSYKEMLESNLLTFNGLANSSAHTHFLDDE 66
QY 125 NYITLLER-KGNGLVCGTNAKRPSCWNLV---NDSVVSLSGM-----KGVAFSPD-E 174
DB 118 NFKIVLQPNQTHLYACGTGAFHVCVCHAVEVGRKSEDNTERLSSFPENGKSPYDKLQ 177
QY 175 NSVLVLEGDEVYSTIRKQENKGIPIPRFRIRGESELT---SDPVMONPQIKATIV-HQ 230
DB 178 TASMLDIG-ELYAGTSDMDFGRDFAIPRTGLKHNPIRTBQDSKWLMDRPFVSHILPES 236
QY 231 DQAYADKIYFFREDNPDKNEAPLNRVAQLCGDGGESSLSVSKWNTFLKAMLVCS 290
DB 237 DNAEDDKIYLFRENAIDGQISKATHARIGQLCKNDFGGHRSL-VAKWTFFLKARLVCS 295

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